

09/529205

Sequence Listing

(110) Sagami Chemical Research Center

5 (120)

(130) 660856

(140)

10 (141)

(150) Japan 9-276271

(151) 1997-10-08

15 (160) 40

(170) Windows 95 (Word 98)

(210) 1

(211) 123

20 (212) PRT

(213) Homo sapiens

(400) 1

(410) 1

(420) 1

(430) 1

Glu Asp Cys Leu Gln Val Lys Asn Cys Thr Gln Leu Gly Glu Gln Cys

35

40

45

Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys

50

55

60

5 Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly

65

70

75

80

Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly

85

90

95

Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala

10

100

105

110

Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu

115

120

15 (210) 2

(211) 220

(212) PRT

(213) Homo sapiens

20 (400) 2

Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly

1

5

10

15

Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser

25

30

35

50 55 60
Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
65 70 75 80
Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val
5 85 90 95
Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala
100 105 110
Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala
115 120 125
10 Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg
130 135 140
Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly
145 150 155 160
Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly
15 165 170 175
Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr
180 185 190
Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala
195 200 205
20 Ser Leu Gly Thr Gly Tyr Asp Arg Lys Asp Tyr Val
210 215 220

<400> 3

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe

1

5

10

15

5 Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro

20

25

30

Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys

35

40

45

Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe

10

50

55

60

Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His Trp

65

70

75

80

Pro

15

<210> 4

<211> 301

<212> PRT

213 Homo sapiens

20

<400> 4

Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg Gly

1

5

10

15

Ala Leu Leu Pro Thr Val Thr Cys Cys Leu Gly Cys Leu Val Gly Arg

Trp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Pro Gly Ile Gly

50

55

60

Gln Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro Ala

65

70

75

80

5 Ala Gly Ala Gly Ala Ala Ala Glu Ala Pro Gly Gly Gln Trp Gly Pro

85

90

95

Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr Ile Pro Asn Met

100

105

110

Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu Ile

10

115

120

125

Ile Glu Glu Asp Phe Asn Ile Ala Leu Gly Val Phe Ala Leu Ala Gly

130

135

140

Leu Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn Trp Ala Asn Gln

145

150

155

160

15 Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile Leu

165

170

175

Ile Ser Ile Leu Tyr Val Ser Leu Thr Tyr Ala Asp Leu Ile Pro Val

180

185

190

Pro Leu Thr Tyr Met Ile Ile Ser Arg Asp Val Met Leu Ile Ala Ala

20

195

200

205

Val Phe Tyr Val Arg Tyr Arg Thr Leu Pro Thr Pro Arg Thr Leu Ala

210

215

220

Lys Tyr Phe Asn Pro Cys Tyr Ala Thr Ala Arg Leu Lys Pro Thr Phe

245

250

255

260

265

270

Leu Trp Cys Phe Thr Ala Phe Thr Thr Ala Ala Ser Ala Tyr Ser Tyr

275

280

285

Tyr His Tyr Gly Arg Lys Thr Val Gln Val Ile Lys Asp

5

290

295

300

210 5

211 383

10 212 PRT

213 Homo sapiens

400 5

Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr

15

1

5

10

15

Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile

20

25

30

Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr

35

40

45

20 Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg

50

55

60

Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro

65

70

75

80

Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg Leu Asp Lys Asp Gly

Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu

115

120

125

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro Asp Arg Cys Glu Ser

130

135

140

5 Cys Tyr Gly Ala Glu Ala Glu Asp Ile Lys Cys Cys Asn Thr Cys Glu

145

150

155

160

Asp Val Arg Glu Ala Tyr Arg Arg Arg Gly Trp Ala Phe Lys Asn Pro

165

170

175

Asp Thr Ile Glu Glu Cys Arg Arg Glu Gly Phe Ser Gln Lys Met Gln

10

180

185

190

Glu Gln Lys Asn Glu Gly Cys Gln Val Tyr Gly Phe Leu Glu Val Asn

195

200

205

Lys Val Ala Gly Asn Phe His Phe Ala Pro Gly Lys Ser Phe Gln Gln

210

215

220

15 Ser His Val His Val His Asp Leu Gln Ser Phe Gly Leu Asp Asn Ile

225

230

235

240

Asn Met Thr His Tyr Ile Gln His Leu Ser Phe Gly Glu Asp Tyr Pro

245

250

255

Gly Ile Val Asn Pro Leu Asp His Thr Asn Val Thr Ala Pro Gln Ala

20

260

265

270

Ser Met Met Phe Gln Tyr Phe Val Lys Val Val Pro Thr Val Tyr Met

275

280

285

Lys Val Asp Gly Glu Val Leu Arg Thr Asn Gln Phe Ser Val Thr Arg

290

300

310

320

325

330

335

Lys His Arg Ser Phe Thr His Phe Leu Thr Gly Val Cys Ala Ile Ile

340

345

350

Gly Gly Met Phe Thr Val Ala Gly Leu Ile Asp Ser Leu Ile Tyr His

5

355

360

365

Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp Leu Gly Lys Thr Thr

370

375

380

10 210 6

211 199

212 PRT

213 Homo sapiens

15 400 6

Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu Asp Pro Ser Phe Val

1

5

10

15

Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu Tyr Trp Asn Val Val

20

25

30

20 Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser Arg Ala Phe Gly Ser

35

40

45

Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Val Thr Ile Leu Leu Leu Asn

50

55

60

Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu Gly Leu Ala Leu

Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe Phe Ala Leu Gly

100

105

110

Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Glv Ile Leu Lys Glu Ala

115

120

125

5 Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn Pro Met Tyr Trp

130

135

140

Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro

145

150

155

160

Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Val Ala

10

165

170

175

Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr Arg Gln Lys Ala

180

185

190

Ser Gly Ser His Lys Arg Ser

195

15

<210> 7

<211> 229

<212> PRT

20 <213> Homo sapiens

<400> 7

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro Trp Ala

35 40 45
Ala Phe Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala Arg Cys
50 55 60
Cys Leu Asn Gln Lys Gly Thr Ile Leu Gly Leu Asp Leu Gln Asn Cys
5 65 70 75 80
Ser Leu Glu Asp Pro Gly Pro Asn Phe His Gln Ala His Thr Thr Val
85 90 95
Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp Leu Ala Asn Thr
100 105 110
10 Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln His Val
115 120 125
Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser Tyr Ile
130 135 140
Asp Asn Gln Ile Cys Gln Gly Gln Lys Asn Leu Cys Asn Asn Thr Gly
15 145 150 155 160
Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp Gly Pro
165 170 175
Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr Lys Cys
180 185 190
20 Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile Leu Gly
195 200 205
Ala Thr Thr Leu Ser Val Ser Ile Leu Leu Trp Ala Thr Gln Arg Arg
210 215 220

<210> 8

<211> 178

<212> PRT

<213> Homo sapiens

5

<400> 8

Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile

1 5 10 15

Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser

10 20 25 30

Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp

35 40 45

Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro

50 55 60

15 Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly

65 70 75 80

Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Lys Ser Thr Lys

85 90 95

Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser

20 100 105 110

Pro Ser Thr Asp Val Gln Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly

115 120 125

Phe His Glu Asp Asp Pro Phe Phe Tyr Asp Glu His Thr Leu Arg Lys

145 150 155 160

165

170

175

Cys Arg

5 (210) 9

(211) 443

(212) PRT

(213) Homo sapiens

10 (400) 9

Met Arg Leu Thr Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr

1

5

10

15

Cys Leu Phe Ser Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg

20

25

30

15 Arg Gln Ala Pro Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala

35

40

45

Pro Ala Arg Glu Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu

50

55

60

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg

20

65

70

75

80

Phe Lys Thr Ser Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr

85

90

95

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu

115

120

125

	130	135	140	
	Ile Thr Gly Pro Ala Val	Ile Pro Gly Tyr Phe Ser Val Asp Val Asn		
	145	150	155	160
	Asn Val Val Leu Ile Leu Asn Gly Arg Glu Lys Ala Lys Ile Phe Tyr			
5	165	170	175	
	Ala Thr Gln Trp Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys			
	180	185	190	
	Leu Gln His Leu Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn			
	195	200	205	
10	Glu Trp Ile Asn Pro Phe Leu Lys Arg Asn Gly Gly Phe Val Glu Leu			
	210	215	220	
	Leu Phe Ile Ile Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe			
	225	230	235	240
	Gln Trp Pro Leu Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu			
15	245	250	255	
	Ala Ser Trp Ser Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe			
	260	265	270	
	Leu Gly Thr Ile Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile			
	275	280	285	
20	Leu Lys Lys Asp Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu			
	290	295	300	
	His Trp Gln Pro Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp			
	305	310	315	320
	Ile Val Tyr Arg Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val			

Val Glu Asp Val Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His

355

360

365

His Gly Ala Pro Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile

370

375

380

5 Phe Ile Lys Asn Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys

385

390

395

400

Thr Ile Ile Leu Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln

405

410

415

Trp Tyr Gln His Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile

10

420

425

430

Leu Glu Ser Ser Phe Leu Met Asn Asn Lys Ser

435

440

15 <210> 10

<211> 130

<212> PRT

<213> Homo sapiens

20 400 10

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu Ser

1

5

10

15

Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu

45

50

55

50 55 60
 Glu Glu Thr Thr Phe Arg Met Glu Ser Asn Leu Tyr Gln Asp Gln Ser
 65 70 75 80
 Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys Arg
 5 85 90 95
 Lys Lys Glu Lys Lys Thr Ala Lys Glu Gly Glu Ser Asn Leu Gly Leu
 100 105 110
 Asp Leu Glu Glu Lys Glu Pro Gly Asp His Glu Arg Ala Lys Ser Thr
 115 120 125
 10 Val Met
 130

(210) 11

15 (211) 369

(212) DNA

(213) Homo sapiens

(400) 11

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 ctgtctgtgt actcctgcaa agcccaggtg agcaacgagg actgcctgca ggtaagaac 120
 tgcaccagc tgggggagca gtgttgacc ggcgcacac ggcagttgg cctcctgacc 180
 gtcacagca aaggttgcag cttgaactgc gtggatgact cacaggacta ctactggggc 240

agccagctc

269

(210) 12

(211) 660

(212) DNA

5 (213) Homo sapiens

(400) 12

atgtccatgg gcttggagat caagggaacc gctgtggcgg tcttgggctg gctgggcacc 60
atctgttgtt gctgttggc catgttggcg gtgttggcct tcatggcag caacatcacc 120
10 acgtctcaga acatctggga gggtctgttg atgaactggc tgggtcagag caccggccag 180
atgcagtga aggtgttaca ctctgtgttg gcactgccac aggaccttca ggctggccgc 240
gcttctatcg tgggtggcat cctgttggc gcttctgggc tcttagtggc gctgttggc 300
gctcagtga ccaactgctt gcaggacgac acggccaagg ccaagatcac catcttggca 360
ggctgtgtgt tcttctctgc cgtctgtctt acctctgttc cgtgttcttg gctggccaac 420
15 accattatcc gggactttta caacctcttg gtgctcgagg cgcagaagcg cgagatgggc 480
gggggctgtt acgttgggtg ggctggcggc gctgtgcagg tcttgggggg cgtctgtctt 540
tctgtctctt gcttctcagg cgcagaagcg tacaaggcca ccaaggctct ctactcggc 600
cgtctctcca cgttctgggg agctcctctt ggcacaggtt acgacctcaa ggaactacgt 660

20

(210) 13

(211) 213

(212) DNA

(400) 1

(213) Homo sapiens

ggcttcttgg tgccttgggt catccctaag ggtccctaacc ggggagttat cattaccaatg 120
 ttgggtgacct gttcagtttg ctgctatctc ttctgggctga ttgcaattct ggccecaactc 180
 aacctctctc ttggaccgca attgaaaaat gaaaccatct ggtatctgaa gtatcattgg 240
 cct 243

5

(210) 14

(211) 903

(212) DNA

10 (213) Homo sapiens

(400) 14

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 ccgggaacgc ggcgagtaa gcgacgcgc tctggggccc tctgcgcgc cgtgcctgc 120
 15 tcttgggct gcctggcga acgtggagg ctgcgtccgg ccgtcttgg cttggcgctg 180
 ccggggatcg gccagcggaa ccaactgttc ggcgctggga aggcggctcc caggccagcg 240
 gccggagcgg gcgcctgc cgaagcccc ggctggcagt ggggccccgc ggcaccccc 300
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 gccccagttc tggctatctt gattatgaa gaagatctta atattgcact aggagtttt 420
 20 gctttagctg gactaacaga ttgttggat ggatttattg ctcgaaacgc ggccaatcaa 480
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 tatgttagct tgacctatgc agatcttatt ccagttccaa ttacttaact gctcatttcg 600
 agagatgtaa tgttgattgc tctgttttt tatgtcagat accgaactct tccaacacca 660
 gtcttcact atgetgacg ctttatctt cagatactat ggtgttta agcttgcgc 840

gac

903

1210 - 15

5 211 - 1149

212 - DNA

213 Homo sapiens

1400 - 15

10	atggaggggc tgggggaagc gaagcagttc gatgcctacc ccaagaattt ggaggacttc	60
	cgggtaaga cctgcggggg cgccaccgtg accattgtca gtggccttct catgetgcta	120
	ctgttctgt cagagetga gtaatacctc accacggagg tgcactctga getctacgtg	180
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	cggcctgagc ttgggaaagt cgaggtagcg gtgtttgacc ctgactccct ggacctgat	420
	cgtgtgaga getgetatgg tgetgagga gaagatata agtgetgtaa cacctgtgaa	480
	gatgtgggg aggcatactc ccttagagga tgggccttca agaaccaga tactattgag	540
	cagtggcggc gagagggctt cagccagaag atgcaggagc agaagaatga aggetgccag	600
20	gtgtatggtc tcttggaagt caataagggt gtcggaaaat tccactttgc ccttggaag	660
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	aacatgacc actacatca gaactgtca ttggggagg actatccagg cattgtgaac	780
	cccttgacc acaccaatgt cactggccc caagctcca tgatgttcca gtactttgtg	840
	gtcttctc tctatgagc ctgcctatg atgggaagc tggggagaa ggcaggctc	900

ctcctcgatt cgtctatcta ccactcagca cgagccatcc agaagaaaat tgatctaggg 1140
 aagacaacg 1149

5 210: 16

211: 597

212: DNA

213: Homo sapiens

10 400: 16

atgaccgggc tgetgggcta cgtggacccc ctggatccca gctttgtggt tgccttcate 60

accatcaccr tcaatecget ctactggaat gtgggtgcac gatgggaaca caagaccgge 120

aagctgagca gggeettggg atccccctac ctggcctgct actctctaaq cgtcaccate 180

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15 atggagagcc tggacacccc cggggcctac agcctggggc tgcgcctctt gggactgggc 300

gtcgtgctcg tgetctccag ctctcttgca ctgggggttc ctggaacttt cctaggtgat 360

tacttgggga tcttcaagga ggcgagagtg accggttcc ccttcaacat cctggacaa 420

cccatgtact ggggaagcac agccaactac ctgggctggg cctcatgca cgcagcccc 480

acgggcttgc tcttgaaggt gctgggtggc ctacactaca tagtggctat cctatacga 540

20 gagcccttca cctgtgagat ctacgggcag aaagcctccg ggtccacaaa gaggaga 597

210: 17

213: Homo sapiens

<400> 17

atggcgcctc acggcccggg tagtcttaag accctgggtgc cctgggctgc cgcctctctc	60
ctcgcctctgg gctgtggaag ggcctctggcg ctaccgcaga tatgcaccca atgtccaggg	120
agcgtgcaaa atttgtaaaa agtggccctt tattgtaaaa cgacacgaga gctaatgtctg	180
catgcccgtt gctgcctgaa tcagaagggc accatcttgg ggcctggatct ccagaactgt	240
tctctggagg accctggtec aaactttcat caggcacata ccactgtcat catagacctg	300
caagcaaac ccctcaaagg tgacttggcc aacaccttc gtggctttac tcagctccag	360
actctgatac tgcacacaac tgtcaactgt cctggaggaa ttaatgcctg gaatactatc	420
acctcttata tagacaacca aatctgtcaa gggcaaaaga accttgcga taacctggg	480
gacccagaaa tgtgtctga gaatggatct tgtgtacctg atggctccagg tcttttgcag	540
tgtgtttgtg ctgatggttt ccattggatac aagtgtatgc gccagggcctc gttctcactg	600
cttatgtctt tggggattct gggagccacc actctatccg tctccattct gctttgggcg	660
accagcgcc gaaaagccaa gacttca	687

15

(210) 18

2115 534

(212) DNA

'213' Homo sapiens

20

4400, 18

atgtcgccct ctggcgccct gtgtcttctc accatcggtg gcctgattct cccaccaga 60

ggacagaagt tgaagatac caggtccagt tcttcagcag actcaactat catggacatt 120

$$\text{Ergodicity} \rightarrow \text{tagging} : \text{AR(1)} \rightarrow \text{ARMA}(1,1) \rightarrow \text{GARCH} \rightarrow \text{IGARCH} \rightarrow \text{GJR} \quad (3.9)$$

5

10

20

geettgcttc agagtgatct cacattgtgc ceggteggag taaacacaga atgetataga 1020
 atctatgagg cttgctccta tggtccatt cctgtggagg aagacgtgat gacagctggc 1080
 aactgtggga atacatctgt gcaccaaggt gctcctctgc agttactcaa gtccatgggt 1140
 gctcccttta tctttatcaa gaactggaag gaactccctg ctgttttaga aaaagagaaa 1200
 5 actataattt tacaagaaaa aattgaaaga agaaaaatgt tacttcagtg gtatcagcac 1260
 ttcaagacag agcttaaaaat gaaatttact aatatttttag aaagctcatt tttaatgaat 1320
 aataaaagt 1329

10 (210) 20

(211) 390

(212) DNA

(213) Homo sapiens

15 (400) 20

atggagaccg tgggggccc tctgggtgctg gagtttctgc tectctcccc ggtggagggc 60
 cagcaggcca cggagcctcg cctgaagccg tggtgggtgg gcttggtctg ggtagctggc 120
 ttcctgttca tctctatatt ggtcttctgc gccaacccgc tctgggttgc caagccagg 180
 gctgaggagc aggaggagac caggttcaga atggagtcca acctatacca ggacccagat 240
 20 gaagacaaga gagagaagaa agaggccatg gagaaagaag agaaggagaa gaaggagaaa 300
 aagacagcaa aggaaggaga gagcaacttg ggactggatc tggaggaaaa agagcccgga 360
 gacctgaga gagcaagag cacagtcctg 390

(11) 979

<213> Homo sapiens

<400> 21

	agcccaccag tgacc atg aag gct gtg ctg ctt gcc ctg ttg atg gca ggc	51
5	Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly	
	1 5 10	
	ttg gcc ctg cag cca ggc act gcc ctg ctg tgc tac tcc tgc aaa gcc	99
	Leu Ala Leu Gln Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala	
	15 20 25	
10	cag gtg agc aac gag gac tgc ctg cag gtg aag aac tgc acc cag ctg	147
	Gln Val Ser Asn Glu Asp Cys Leu Gln Val Lys Asn Cys Thr Gln Leu	
	30 35 40	
	ggg gag cag tgc tgg acc ggc cgc atc cgc gca gtt ggc ctc ctg acc	195
	Gly Glu Gln Cys Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr	
15	45 50 55 60	
	gtc atc agc aaa ggc tgc agc ttg aac tgc gtg gat gac tca cag gac	243
	Val Ile Ser Lys Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp	
	65 70 75	
	tac tac gtg ggc aag aag aac atc aag tgc tgt gac acc gac ttg tgc	291
20	Tyr Tyr Val Gly Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys	
	80 85 90	
	aac gcc agc ggg gcc cat gcc ctg cag cag gct gcc gcc atc ctt gag	339
	Asn Ala Ser Gly Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala	
	Leu Leu Pro Ala Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu	

tagget ctggggggcc ccgtgcagc ccacactggg tgtggtgccc caggectctg 440
 tgcacactct cacagacctg gccagtgagg agcctgtctt ggttcttgag gcacatccta 500
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 tctccaggac tcccaccgg cagatcagct ctagtgcac agatccgctt gcagatggcc 620
 5 cctccaaacc tctctgtctg tgtttccatg gccagcatt ctccacctt aacctgtgc 680
 tcaggacct ctcccccag gaagccttc ctgccacc cctctatgac ttgagccagg 740
 tctggctcgt ggtgtccccc gcaccacga ggggacagge actcaggagg gccagtaaa 800
 ggctgagatg aagtggactg agtagaactg gaggacaaga gtgcagtgga gtctctggga 860
 gtctccagag atggggcctg gaggcctgga ggaaggggccc aggcctcaca ttcgtggggc 920
 10 tccctgaatg gcagcctgag cacagcgtag gcccttaata aacacctgtt ggataagcc 979

<210> 22

<211> 123

15 <212> PRT

<213> Homo sapiens

<400> 22

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly

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Leu Ala Leu Gln Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala

15

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25

Gln Val Ser Asn Glu Asp Cys Leu Gln Val Lys Asn Cys Thr Gln Leu

45

50

55

60

65 70 75
 Tyr Tyr Val Gly Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys
 80 85 90
 Asn Ala Ser Gly Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala
 5 95 100 105
 Leu Leu Pro Ala Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
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10 (210) 23
 (211) 1279
 (212) DNA
 (213) Homo sapiens

15 (400) 23
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 cgcgcgcgcg gtcgggggcg cgcagctccc gccagggccc gggggccggg cgcgcgcgcg 180
 cgcgcgcgcg ggagccaccc ggtggagcgg gcctggcgcg ggcagcc atg tcc atg 236

20 Met Ser Met
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 ggc ctg gag atc acg ggc acc ggc ctg gcc gtc ctg ggc tgg ctg gcc 284
 Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly Trp Leu Gly

Ile Ile Val Lys Cys Ala Leu Pro Met Trp Arg Val Ser Ala Ile Ile

ggc agc aac atc atc acg teg cag aac atc tgg gag ggc ctg tgg atg 380
 Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly Leu Trp Met
 40 45 50
 aac tgc gtg gtg cag agc acc ggc cag atg cag tgc aag gtg tac gac 428
 5 Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys Val Tyr Asp
 55 60 65
 teg ctg ctg gca ctg cca cag gac ctt cag ggc gcc cgc gcc ctc atc 476
 Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala Leu Ile
 70 75 80
 10 gtg gtg gcc atc ctg ctg gcc gcc ttc ggg ctg cta gtg ggc ctg gtg 524
 Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val Ala Leu Val
 85 90 95
 ggc gcc cag tgc acc aac tgc gtg cag gac gac acg gcc aag gcc aag 572
 Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala Lys Ala Lys
 15 100 105 110 115
 atc acc atc gtg gca ggc gtg ctg ttc ctt ctc gcc gcc ctg ctc acc 620
 Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala Leu Leu Thr
 120 125 130
 ctg gtg cgg gtg tcc tgg teg gcc aac acc att atc cgg gac ttc tac 668
 20 Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg Asp Phe Tyr
 135 140 145
 aac ccc gtg gtg ccc gag gcc cag aag cgc gag atg gcc gcc gcc ctg 716
 Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly Ala Gly Leu
 150 155 160 165 170 175 180
 tyr val gly trp ala ala ala ala leu gln leu leu gly gly ala leu

etc tgc tgc teg tgt ccc cca cgc gag aag aag tac acg gcc acc aag 812
 Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr Ala Thr Lys
 180 185 190 195
 gtc gtc tac tcc gcg ccg cgc tcc acc gcc cgg gga gcc agc ctg gcc 860
 5 Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala Ser Leu Gly
 200 205 210
 aca gcc tac gac cgc aag gac tac gtc taa gggacagacg cagggagacc 910
 Thr Gly Tyr Asp Arg Lys Asp Tyr Val
 215 220
 10 ccaccaccac caccaccacc aacaccacca ccaccacagc gagctggagc ggcaccagg 970
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20 <211> 220

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<213> Homo sapiens

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Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly Leu Trp Met
5 40 45 50
Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys Val Tyr Asp
55 60 65
Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala Leu Ile
70 75 80
10 Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val Ala Leu Val
85 90 95
Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala Lys Ala Lys
100 105 110 115
Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala Leu Leu Thr
15 120 125 130
Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg Asp Phe Tyr
135 140 145
Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly Ala Gly Leu
150 155 160
20 Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly Gly Ala Leu
165 170 175
Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr Ala Thr Lys
180 185 190 195
Ile Ile Tyr Asp Arg Asn Asn Tyr Val
200 205

<210> 25

<211> 835

5 <212> DNA

<213> Homo sapiens

<400> 25

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Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val

1 5 10 15

ttc tgg ggc ttc gtc ggc ttc ttg gtg cct tgg ttc atc cct aag ggt 155

Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly

15 20 25 30

cct aac cgg gga gtt atc att acc atg ttg gtg acc tgt tca gtt tgc 203

Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys

35 40 45

tgc tat ctc ttt tgg ctg att gca att ctg ggc caa ctc aac cct ctc 251

20 Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu

50 55 60

ttt gga cgg caa ttg aaa aat gaa acc atc tgg tat ctg aag tat cat 299

Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His

Trp Trp

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 5 ctgagagata cgttactctc tccttggaat ctgtggattt gaagatgget cctgccttct 650
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 tatgg 835

10

210 > 26

211 > 81

212 > PRT

15 213 > Homo sapiens

400 > 26

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val

1

5

10

15

20 Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly

20

25

30

Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys

35

40

45

Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His

Trp Pro

80

5 (210) 27

(211) 1256

(212) DNA

(213) Homo sapiens

10 (400) 27

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ggcc atg cta gcc ttg cgc gtg ggc cgc ggc tgc tgg ggg gcc ctg cgc 169

Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg

15 1 5 10 15

ggc gcc gct tgg gct ccg gga acg cgg ccg agt aag cga cgc gcc tgc 217

Gly Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg Arg Ala Cys

20 25 30

tgg gcc ctg ctg ccg ccc gtg ccc tgc tgc ttg ggc tgc ctg gcc gaa 265

20 Trp Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu

35 40 45

cgc tgg agg ctg cgt ccg gcc gct ctt ggc ttg cgg ctg ccc ggg atc 313

Arg Trp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Pro Gly Ile

Gly Gln Arg Asn His Trp Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro

gcg gcc gga gcg ggc gcc gct gcc gaa gcc cgg ggc ggc cag tgg ggc 409
 Ala Ala Gly Ala Gly Ala Ala Ala Glu Ala Pro Gly Gly Gln Trp Gly
 80 85 90 95
 ccg gcg agc acc ccc agc ctg tat gaa aac cca tgg aca atc ccg aat 457
 5 Pro Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr Ile Pro Asn
 100 105 110
 atg ttg tca atg acg aga att ggc ttg gcc cca gtt ctg ggc tat ttg 505
 Met Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu
 115 120 125
 10 att att gaa gaa gat ttt aat att gca cta gga gtt ttt gct tta gct 553
 Ile Ile Glu Glu Asp Phe Asn Ile Ala Leu Gly Val Phe Ala Leu Ala
 130 135 140
 gga cta aca gat ttg ttg gat gga ttt att gct cga aac tgg gcc aat 601
 Gly Leu Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn Trp Ala Asn
 15 145 150 155
 caa aga tca gct ttg gga agt gct ctt gat cca ctt gct gat aaa ata 649
 Gln Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile
 160 165 170 175
 ctt atc agt atc tta tat gtt agc ttg acc tat gca gat ctt att cca 697
 20 Leu Ile Ser Ile Leu Tyr Val Ser Leu Thr Tyr Ala Asp Leu Ile Pro
 180 185 190
 gtt cca ctt act tac atg atc att tgg aga gat gta atg ttg att gct 745
 Val Pro Leu Thr Tyr Met Ile Ile Ser Arg Asp Val Met Leu Ile Ala
 Ala Val Phe Tyr Val Arg Tyr Arg Thr Leu Thr Thr Pro Arg Thr Leu

gcc aag tat ttc aat cct tgc tat gcc act get agg tta aaa cca aca 841
 Ala Lys Tyr Phe Asn Pro Cys Tyr Ala Thr Ala Arg Leu Lys Pro Thr
 225 230 235
 ttc atc agc aag gtg aat aca gca gtc cag tta atc ttg gtg gca get 889
 5 Phe Ile Ser Lys Val Asn Thr Ala Val Gln Leu Ile Leu Val Ala Ala
 240 245 250 255
 tct ttg gca get cca gtt ttc aac tat get gac age att tat ctt cag 937
 Ser Leu Ala Ala Pro Val Phe Asn Tyr Ala Asp Ser Ile Tyr Leu Gln
 260 265 270
 10 ata cta tgg tgt ttt aca get ttc aac aca get gca tca get tat agt 985
 Ile Leu Trp Cys Phe Thr Ala Phe Thr Thr Ala Ala Ser Ala Tyr Ser
 275 280 285
 tac tat cat tat ggc egg aag act gtt cag gtg ata aaa gac tga 1030
 Tyr Tyr His Tyr Gly Arg Lys Thr Val Gln Val Ile Lys Asp
 15 290 295 300
 tgaaagtcac cctcactgt tagtaaggaa gcagtataca tcaatgggaa cagggeccat 1090
 ggaaatgtac aggagtctcc ctatttttgt gtccagcttg aaaaaggact tgcagaate 1150
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<210> 28

<211> 301

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Gly Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg Arg Ala Cys

20 25 30

5 Trp Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu

35 40 45

Arg Trp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Pro Gly Ile

50 55 60

Gly Gln Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro

10 65 70 75

Ala Ala Gly Ala Gly Ala Ala Ala Glu Ala Pro Gly Gly Gln Trp Gly

80 85 90 95

Pro Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr Ile Pro Asn

100 105 110

15 Met Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu

115 120 125

Ile Ile Glu Glu Asp Phe Asn Ile Ala Leu Gly Val Phe Ala Leu Ala

130 135 140

Gly Leu Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn Trp Ala Asn

20 145 150 155

Gln Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile

160 165 170 175

Leu Ile Ser Ile Leu Tyr Val Ser Leu Thr Tyr Ala Asp Leu Ile Pro

180

185

190

220

—

235

255

270

285

300

51

10

99

147

	30	35	40	
	ctg tcc gag ctg cag tat tac ctc acc acg gag gtg cat cct gag ctc	195		
	Leu Ser Glu Leu Gln Tyr Tyr Leu Thr Thr Glu Val His Pro Glu Leu			
	45	50	55	
5	tac gtg gac aag teg cgg gga gat aaa ctg aag atc aac atc gat gta	243		
	Tyr Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val			
	60	65	70	
	ctt ttt cgg cac atg cct tgt gcc tat ctg agt att gat gcc atg gat	291		
	Leu Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp			
10	75	80	85	90
	gtg gcc gga gaa cag cag ctg gat gtg gaa cac aac ctg ttc aag caa	339		
	Val Ala Gly Glu Gln Gln Leu Asp Val Glu His Asn Leu Phe Lys Gln			
	95	100	105	
	cga cta gat aaa gat ggc atc ccc gtg agc tca gag gct gag cgg cat	387		
15	Arg Leu Asp Lys Asp Gly Ile Pro Val Ser Ser Glu Ala Glu Arg His			
	110	115	120	
	gag ctt ggg aaa gtc gag gtg acg gtg ttt gac cct gac tcc ctg gac	435		
	Glu Leu Gly Lys Val Glu Val Thr Val Phe Asp Pro Asp Ser Leu Asp			
	125	130	135	
20	cct gtt cgc tgt gag agc tgc tat ggt gct gag gca gaa gat atc aag	483		
	Pro Asp Arg Cys Glu Ser Cys Tyr Gly Ala Glu Ala Glu Asp Ile Lys			
	140	145	150	
	tgc tgt aac acc tgt gaa gat gtg cgg gag gca tat cgc cgt aga ggc	531		
	tgg gct ttt atg aa tca ggt att att gac cag tg tgg cca gag ggc	579		

	175	180	185	
	ttc agc cag aag atg cag gag cag aag aat gaa ggc tgc cag gtg tat	627		
	Phe Ser Gln Lys Met Gln Glu Gln Lys Asn Glu Gly Cys Gln Val Tyr			
	190	195	200	
5	ggc ttc ttg gaa gtc aat aag gtg gcc gga aac ttc cac ttt gcc cct	675		
	Gly Phe Leu Glu Val Asn Lys Val Ala Gly Asn Phe His Phe Ala Pro			
	205	210	215	
	ggg aag agc ttc cag cag tcc cat gtg cac gtc cat gac ttg cag agc	723		
	Gly Lys Ser Phe Gln Gln Ser His Val His Val His Asp Leu Gln Ser			
10	220	225	230	
	ttt ggc ctt gac aac atc aac atg acc cac tac atc cag cac ctg tca	771		
	Phe Gly Leu Asp Asn Ile Asn Met Thr His Tyr Ile Gln His Leu Ser			
	235	240	245	250
	ttt ggg gag gac tat cca ggc att gtg aac ccc ctg gac cac acc aat	819		
15	Phe Gly Glu Asp Tyr Pro Gly Ile Val Asn Pro Leu Asp His Thr Asn			
	255	260	265	
	gtc act ggc ccc caa gcc tcc atg atg ttc cag tac ttt gtg aag gtg	867		
	Val Thr Ala Pro Gln Ala Ser Met Met Phe Gln Tyr Phe Val Lys Val			
	270	275	280	
20	gtg ccc act gtg tac atg aag gtg gac gga gag gta ctg agg aca aat	915		
	Val Pro Thr Val Tyr Met Lys Val Asp Gly Glu Val Leu Arg Thr Asn			
	285	290	295	
	cag tta tct gtg acc aga cat gag aag gtt gcc aat ggg ctg ttg ggc	963		
	gac cag gcc ttt ccc gga gtc tta gtc ttc aat gag ttt t gac atg	1011		

315 320 325 330
atg gtg aag ctg acg gag aag cac agg tcc ttc acc cac ttc ctg aca 1059

Met Val Lys Leu Thr Glu Lys His Arg Ser Phe Thr His Phe Leu Thr

335 340 345

5 ggt gtg tgc gcc atc att ggg ggc atg ttc aca gtg gct gga ctc atc 1107

Gly Val Cys Ala Ile Ile Gly Gly Met Phe Thr Val Ala Gly Leu Ile

350 355 360

gat tgg ctc atc tac cac tca gca cga gcc atc cag aag aaa att gat 1155

Asp Ser Leu Ile Tyr His Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp

10 365 370 375

cta ggg aag aca acg tagtcacct cgggtgcttcc tctgtctcct cttctctcct 1210

Leu Gly Lys Thr Thr

380

ggcctgtggt tgteccccag cctctgccac cctccacctc ctcggtcagc cccagcccca 1270

15 gggtgataaaa tetattgatt gattgtgata gtaac 1305

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<211> 383

20 <212> PRT

<213> Homo sapiens

<400> 30

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Gly Ala Thr Val Thr Ile Val Ser Gly Leu Leu Met Leu Leu Leu Phe

30

35

40

Leu Ser Glu Leu Gln Tyr Tyr Leu Thr Thr Glu Val His Pro Glu Leu

45

50

55

5 Tyr Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val

60

65

70

Leu Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp

75

80

85

90

Val Ala Gly Glu Gln Gln Leu Asp Val Glu His Asn Leu Phe Lys Gln

10

95

100

105

Arg Leu Asp Lys Asp Gly Ile Pro Val Ser Ser Glu Ala Glu Arg His

110

115

120

Glu Leu Gly Lys Val Glu Val Thr Val Phe Asp Pro Asp Ser Leu Asp

125

130

135

15 Pro Asp Arg Cys Glu Ser Cys Tyr Gly Ala Glu Ala Glu Asp Ile Lys

140

145

150

Cys Cys Asn Thr Cys Glu Asp Val Arg Glu Ala Tyr Arg Arg Arg Gly

155

160

165

170

Trp Ala Phe Lys Asn Pro Asp Thr Ile Glu Gln Cys Arg Arg Gln Gly

20

175

180

185

Phe Ser Gln Lys Met Gln Glu Gln Lys Asn Glu Gly Cys Gln Val Tyr

190

195

200

Gly Phe Leu Glu Val Asn Lys Val Ala Gly Asn Phe His Phe Ala Pro

235 240 245 250

Phe Gly Glu Asp Tyr Pro Gly Ile Val Asn Pro Leu Asp His Thr Asn

255 260 265

Val Thr Ala Pro Gln Ala Ser Met Met Phe Gln Tyr Phe Val Lys Val

5 270 275 280

Val Pro Thr Val Tyr Met Lys Val Asp Gly Glu Val Leu Arg Thr Asn

285 290 295

Gln Phe Ser Val Thr Arg His Glu Lys Val Ala Asn Gly Leu Leu Gly

300 305 310

10 Asp Gln Gly Leu Pro Gly Val Phe Val Leu Tyr Glu Leu Ser Pro Met

315 320 325 330

Met Val Lys Leu Thr Glu Lys His Arg Ser Phe Thr His Phe Leu Thr

335 340 345

Gly Val Cys Ala Ile Ile Gly Gly Met Phe Thr Val Ala Gly Leu Ile

15 350 355 360

Asp Ser Leu Ile Tyr His Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp

365 370 375

Leu Gly Lys Thr Thr

380

20

<210> 31

211 - 899

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Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu Asp

1 5 10

5 ccc agc ttt gtg gct gcc gtc atc acc atc acc ttc aat ccg etc tac 157

Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu Tyr

15 20 25

tgg aat gfg gtt gca cga tgg gaa cac aag acc cgc aag ctg agc agg 205

Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser Arg

10 30 35 40

gac ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc gtc acc atc 253

Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Val Thr Ile

45 50 55 60

ctg ctc ctg aac ttc ctg cgc tgg cac tgc ttc acg cag gcc atg ctg 301

15 Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu

65 70 75

agc cag ccc agg atg gag agc ctg gac acc ccc ggc gcc tac agc ctg 349

Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu

80 85 90

20 *ggc att ggg ctc ctg gga ctg ggc gtc gtc att g'g att att ggc tt* 407

Gly Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe

95 100 105

ttt gga ctg ggg ttg gct gga act ttg cta ggt gat tac ttg ggg atc 445

[illegible]

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	ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg gcc atc atg	541			
	Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met				
	145	150	155		
5	cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg gcc ctc acc	589			
	His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr				
	160	165	170		
	tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct gag atc tac	637			
	Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr				
10	175	180	185		
	egg cag aaa gcc tcc ggg tcc cac aag agg agc tgattgagct gcaacagctt	690			
	Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser				
	190	195			
	tgtctgaaggc ctggccagcc tcttggcctg ccccaagtgg cagggcctgc gcagggcgag	750			
15	aatgggtgcct gctgctcagg gctcgcctcc ggctgtgggt gccccagtgc cttggaacct	810			
	gctgccttgg ggaccttga cgtgcgcaca tatggccatt gagctccaac ccacacattc	870			
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20	210- 32				
	211- 199				
	<212> PRT				
	<213> Homo sapiens				

Met Thr Arg Leu Leu Leu Leu Thr Val Ala Thr Thr Thr Thr

Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu Tyr
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Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser Arg
30 35 40
5 Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Val Thr Ile
45 50 55 60
Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu
65 70 75
Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu
10 80 85 90
Gly Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe
95 100 105
Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile
110 115 120
15 Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn
125 130 135 140
Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met
145 150 155
His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr
20 160 165 170
Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr
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<211> 905

<212> DNA

<213> Homo sapiens

5 <400> 33

aacggaaa atg gcg cct cac ggc cgg ggt agt ctt acg acc ctg gtg ccc 50

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro

1 5 10

tgg get gcc gcc ctg ctc ctc get ctg ggc gtg gaa agg get ctg geg 98

10 Trp Ala Ala Ala Leu Leu Leu Ala Leu Gly Val Glu Arg Ala Leu Ala

15 20 25 30

cta ccc gag ata tgc acc caa tgt cca ggg agc gtg caa aat ttg tca 146

Leu Pro Glu Ile Cys Thr Gln Cys Pro Gly Ser Val Gln Asn Leu Ser

35 40 45

15 aaa gtg gcc ttt tat tgt aaa acg aca cga gag cta atg ctg cat gcc 194

Lys Val Ala Phe Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala

50 55 60

cgt tgc tgc ctg aat cag aag ggc acc atc ttg ggg ctg gat ctc cag 242

Arg Cys Cys Leu Asn Gln Lys Gly Thr Ile Leu Gly Leu Asp Leu Gln

20 65 70 75

aac tgt tet ctg gag gac cct ggt cca aac ttt cat cag gca cat acc 290

Asn Cys Ser Leu Glu Asp Pro Gly Pro Asn Phe His Gln Ala His Thr

80 85 90

95

100

105

110

Asn Thr Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln

115

120

125

cat gtc aac tgt cct gga gga att aat gcc tgg aat act atc acc tct 434

His Val Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser

5

130

135

140

tat ata gac aac caa atc tgt caa ggg caa aag aac ctt tgc aat aac 482

Tyr Ile Asp Asn Gln Ile Cys Gln Gly Gln Lys Asn Leu Cys Asn Asn

145

150

155

act ggg gac cca gaa atg tgt cct gag aat gga tct tgt gta cct gat 530

10 Thr Gly Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp

160

165

170

ggc cca ggt ctt ttg cag tgt gtt tgt gct gat ggt ttc cat gga tac 578

Gly Pro Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr

175

180

185

190

15 aag tgt atg cgc cag ggc tgg ttc tca ctg ctt atg ttc ttc ggg att 626

Lys Cys Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile

195

200

205

ctg gga gcc acc act cta tcc gtc tcc att ctg ctt tgg ggc acc cag 674

Leu Gly Ala Thr Thr Leu Ser Val Ser Ile Leu Leu Trp Ala Thr Gln

20

210

215

220

cgc cga aaa gcc aag act tca tgaac tacatagggc ttaccattga 720

Arg Arg Lys Ala Lys Thr Ser

225

CTG GGA GCC ACC ACT CTA TCC GTC TCC ATT CTG CTT TGG GGC ACC CAG 867

(210) 34

(211) 229

5 (212) PRT

(213) Homo sapiens

(400) 34

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro

10 1 5 10

Trp Ala Ala Ala Leu Leu Leu Ala Leu Gly Val Glu Arg Ala Leu Ala

15 20 25 30

Leu Pro Glu Ile Cys Thr Gln Cys Pro Gly Ser Val Gln Asn Leu Ser

35 40 45

15 Lys Val Ala Phe Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala

50 55 60

Arg Cys Cys Leu Asn Gln Lys Gly Thr Ile Leu Gly Leu Asp Leu Gln

65 70 75

Asn Cys Ser Leu Glu Asp Pro Gly Pro Asn Phe His Gln Ala His Thr

20 80 85 90

Thr Val Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp Leu Ala

95 100 105 110

Asn Thr Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln

145 150 155
 Thr Gly Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp
 160 165 170
 Gly Pro Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr
 5 175 180 185 190
 Lys Cys Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile
 195 200 205
 Leu Gly Ala Thr Thr Leu Ser Val Ser Ile Leu Leu Trp Ala Thr Gln
 210 215 220
 10 Arg Arg Lys Ala Lys Thr Ser
 225

(210) 35

15 (211) 841

(212) DNA

(213) Homo sapiens

(400) 35

20 atccdegagg ctgcgggatt aggaacccca gctccgac atg tgg cca t t ggt cgc 50

Met Ser Pro Ser Gly Arg

1 5

ctg tgt ctt ctc acc atc gtt ggc ctg att ctc ccc acc aga gga cag 104

ccg ttc aag ggt att tgc ttc agt ttc tca gaa ggt ttc ttc ttc ttc 15

	25	30	35	
	gac att cag gtc ceg aca cga gcc cca gat gca gtc tac aca gaa etc			200
	Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr Glu Leu			
	40	45	50	
5	cag ccc acc tct cca acc cca acc tgg cct gct gat gaa aca cca caa			248
	Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr Pro Gln			
	55	60	65	70
	ccc cag acc cag acc cag cca ctg gaa gga acg gat ggg cct cta gtg			296
	Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro Leu Val			
10	75	80	85	
	aca gat cca gag aca cac aag agc acc aaa gca gct cat ccc act gat			344
	Thr Asp Pro Glu Thr His Lys Ser Thr Lys Ala Ala His Pro Thr Asp			
	90	95	100	
	gac acc acg acg etc tct gag aga cca tcc cca agc aca gac gtc cag			392
15	Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Asp Val Gln			
	105	110	115	
	aca gac ccc cag acc etc aag cca tct ggt ttt cat gag gat gac ccc			440
	Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly Phe His Glu Asp Asp Pro			
	120	125	130	
20	ttc ttc tat gat gaa cac acc etc egg aaa egg ggg ctg ttg gtc gca			488
	Phe Phe Tyr Asp Glu His Thr Leu Arg Lys Arg Gly Leu Leu Val Ala			
	135	140	145	150
	gct gtg ctg ttc atc aca ggc atc atc atc etc acc agt ggc aag tgc			536
	agg cag etc ttc egg tta ttc egg aat cat ttc agg tggc ca			580

170

175

tcagaaacag gagctgacaa cccgctgggc acccgaagac caageccccct gccagctcac 640
 cgtgcccagc ctctgcac cccctgaaga gcttgccag agagggaaga cacagatgat 700
 gaagctggag ccagggtgc cggctcagat ctctaccc ccccaacct gccgccccct 760
 5 gaaggetacc tggcgcttg ggggetgtcc ctcaagtat ctctctgtt aagacaaaaa 820
 gtaaagcact gtggtctttg c 841

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10 <211> 178

<212> PRT

<213> Homo sapiens

<400> 36

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Met Ser Pro Ser Gly Arg

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5

Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg Gly Gln

10

15

20

Thr Leu Lys Asp Thr Thr Ser Ser Ser Ala Asp Ser Thr Ile Met

20

25

30

35

Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr Glu Leu

40

45

50

Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr Pro Gln

75

80

85

	90	95	100
	Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Asp Val Gln		
	105	110	115
	Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly Phe His Glu Asp Asp Pro		
5	120	125	130
	Phe Phe Tyr Asp Glu His Thr Leu Arg Lys Arg Gly Leu Leu Val Ala		
	135	140	145 150
	Ala Val Leu Phe Ile Thr Gly Ile Ile Ile Leu Thr Ser Gly Lys Cys		
	155	160	165
10	Arg Gln Leu Ser Arg Leu Cys Arg Asn His Cys Arg		
	170	175	

(210) 37

15 (211) 1451

(212) DNA

(213) Homo sapiens

(400) 37

20 actgcectgga aacgggetgg gectgcectg gacgecgccg gtgtcgcgga ttctcttcc 60
gcccgtcca tggcggtgga tgcctgactg gaagcccgag tggg atg cgg ctg acg 110

Met Arg Leu Thr

1

Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg Arg Gln Ala Pro

25

30

35

gcc ggg tcc ccg cgg ggc ctc agg aag ggg gcg gcc ccc gcg cgg gag 260

Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala Pro Ala Arg Glu

5

40

45

50

aga cgc ggc cga gaa cag tcc act ttg gaa agt gaa gaa tgg aat cct 308

Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu Glu Trp Asn Pro

55

60

65

tgg gaa gga gat gaa aaa aat gag caa caa cac aga ttt aaa act age 355

10 Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg Phe Lys Thr Ser

70

75

80

ctt caa ata tta gat aaa tcc acg aaa gga aaa aca gat ctc agt gta 404

Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr Asp Leu Ser Val

85

90

95

100

15 caa atc tgg ggc aaa get gcc att ggc tgg tat ctc tgg gag cat att 452

Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu Trp Glu His Ile

105

110

115

ttt gaa ggc tta ctt gat ccc agc gat gtg act get caa tgg aga gaa 500

Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala Gln Trp Arg Glu

20

120

125

130

gga aag tca atc gta gga aga aca cag tac agc ttc atc act ggt cca 548

Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe Ile Thr Gly Pro

135

140

145

150

155

160

ile leu asn gly arg glu lys ala lys ile phe tyr ala thr gln trp

165 170 175 180

tta ctt tat gca caa aat tta gtg caa att caa aaa ctc cag cat ctt 692

Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys Leu Gln His Leu

5 185 190 195

gct gtt gtt ttg ctc gga aat gaa cat tgt gat aat gag tgg ata aac 740

Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn Glu Trp Ile Asn

200 205 210

cca ttc ctc aaa aga aat gga ggc ttc gtg gag ctg ctt ttc ata ata 788

10 Pro Phe Leu Lys Arg Asn Gly Gly Phe Val Glu Leu Leu Phe Ile Ile

215 220 225

tat gac agc ccc tgg att aat gac gtg gat gtt ttt cag tgg cct tta 836

Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe Gln Trp Pro Leu

230 235 240

15 gga gta gca aca tac agg aat ttt cct gtg gtg gag gca agt tgg tca 884

Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Trp Ser

245 250 255 260

atg ctg cat gat gag agg cca tat tta tgt aat ttc tta gga acg att 932

Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile

20 265 270 275

tat gaa aat tca tcc aga cag gca cta atg aac att ttg aaa aaa gat 980

Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp

280 285 290

Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln
 310 315 320

agt gat ctc aca ttg tgc ccg gtc gga gta aac aca gaa tgc tat cga 1124
 Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg

5 325 330 335 340
 atc tat gag gct tgc tcc tat ggc tcc att cct gtg gtg gaa gac gtg 1172
 Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val Val Glu Asp Val

345 350 355
 atg aca gct ggc aac tgt ggg aat aca tct gtg cac cac ggt gct cct 1220
 10 Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His His Gly Ala Pro

360 365 370
 ctg cag tta ctc aag tcc atg ggt gct ccc ttt atc ttt atc aag aac 1268
 Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn

375 380 385
 15 tgg aag gaa ctc cct gct gtt tta gaa aaa gag aaa act ata att tta 1316
 Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu

390 395 400
 caa gaa aaa att gaa aga aga aaa atg tta ctt cag tgg tat cag cac 1364
 Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His

20 405 410 415 420
 ttc aag aca gag ctt aaa atg aaa ttt act aat att tta gaa agc tca 1412
 Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser

425 430 435

<210> 38

211 443

<212> PRT

5 <213> Homo sapiens

<400> 38

Met Arg Leu Thr

i

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5 10 15 20

Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg Arg Gln Ala Pro

25 30 35

Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala Pro Ala Arg Glu

15 40 45 50

Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu Glu Trp Asn Pro

55 60 65

Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg Phe Lys Thr Ser

70 75 80

20 Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr Asp Leu Ser Val

85 90 95 100

Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu Trp Glu His Ile

105 110 115

Gly Lys Ser Ile Val Arg Arg Thr Gln Tyr Ser Ile Ile Thr Tyr Trp

Ala Val Ile Pro Gly Tyr Phe Ser Val Asp Val Asn Asn Val Val Leu

150

155

160

Ile Leu Asn Gly Arg Glu Lys Ala Lys Ile Phe Tyr Ala Thr Gln Trp

165

170

175

180

5 Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys Leu Gln His Leu

185

190

195

Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn Glu Trp Ile Asn

200

205

210

Pro Phe Leu Lys Arg Asn Gly Gly Phe Val Glu Leu Leu Phe Ile Ile

10

215

220

225

Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe Gln Trp Pro Leu

230

235

240

Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Trp Ser

245

250

255

260

15 Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile

265

270

275

Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp

280

285

290

Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu His Trp Gln Pro

20

295

300

305

Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln

310

315

320

Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg

345

350

355

360 365 370
 Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn
 375 380 385
 Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu
 5 390 395 400
 Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His
 405 410 415 420
 Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser
 425 430 435
 10 Phe Leu Met Asn Asn Lys Ser
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<210> 39

15 <211> 886

<212> DNA

<213> Homo sapiens

<400> 39

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 tc atg gag acc ctg ggg gcc ctt ctg gtg ctg gag ttt ctg etc etc 107
 Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu
 1 5 10 15

20

25

30

Leu Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu

35

40

45

gtc ttg ctg gcc aac cgc ctc tgg tgt tcc aag gcc agg gct gag gac 251

Val Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp

5

50

55

60

gag gag gag acc acg ttc aga atg gag tcc aac cta tac cag gac cag 299

Glu Glu Glu Thr Thr Phe Arg Met Glu Ser Asn Leu Tyr Gln Asp Gln

65

70

75

agt gaa gac aag aga gag aag aaa gag gcc aag gag aaa gaa gag aag 347

10 Ser Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys

80

85

90

95

agg aag aag gag aaa aag aca gca aag gaa gga gag agc aac ttg gga 395

Arg Lys Lys Glu Lys Lys Thr Ala Lys Glu Gly Glu Ser Asn Leu Gly

100

105

110

15 ctg gat ctg gag gaa aaa gag ccc gga gac cat gag aga gca aag agc 443

Leu Asp Leu Glu Glu Lys Glu Pro Gly Asp His Glu Arg Ala Lys Ser

115

120

125

aca gtc atg tgaagatt cctggetgce tcttccagge agtccccag agatgcctct 500

Thr Val Met

20

130

tctgccccct aaaagcagtg cccctggactt gaagcccgctg aaatgaactcc atctgggatt 560

cagaatacag tgtttctcaag tgaagaagge ttggaaccca ccccacctcc ctcattgggg 620

gctctctggg caaacatggt ttctcatgcac cctcttctct gagcttgggc cctgcctggc 680

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<211> 130

5 <212> PRT

<213> Homo sapiens

<400> 40

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu

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Ser Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp

 20 25 30

Leu Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu

 35 40 45

15 Val Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp

 50 55 60

Glu Glu Glu Thr Thr Phe Arg Met Glu Ser Asn Leu Tyr Gln Asp Gln

 65 70 75

Ser Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys

20 80 85 90 95

Arg Lys Lys Glu Lys Lys Thr Ala Lys Glu Gly Glu Ser Asn Leu Gly

 100 105 110

Leu Asp Leu Glu Glu Lys Glu Pro Gly Asp His Glu Arg Ala Lys Ser